



(B)

Wed Nov 21 09:32:15 2001 [BLASTP 2.2.1 [Jul-12-2001], NCBI]
/home/ruby/va/Molbio/carpenda/tempblast/p1.DNA59606.nc (477 aa)

BLAST RESULTS B-1

Sequences producing High-scoring Segment Pairs:				Score	Match	Pct	E-val
1	P_AAB65239	Human PRO1107 (UNQ550) protein sequence S		2561	477	100	0.0
2	P_AAU12397	Human PRO1107 polypeptide sequence - Homo		2561	477	100	0.0
3	P_AAY66716	Membrane-bound protein PRO1107 - Homo sap		2561	477	100	0.0
4	P_AAB24072	Human PRO1107 protein sequence SEQ ID NO:		2561	477	100	0.0
5	P_AAE05491	Human phosphodiesterase-1 (HPDE-1) - Homo		2553	475	100	0.0
6	CAB56566.1	dJ8B1.3 (similar to PLASMA-CELL MEMBRANE		2551	474	99	0.0
7	NP_067547.1	ectonucleotide pyrophosphatase/phosphodie		2551	474	99	0.0
8	A59391	probable phosphodiesterase I (EC 3.1.4.1)		2551	474	99	0.0
9	P_AAM23765	Human EST encoded protein SEQ ID NO: 1290		2403	446	99	0.0

>1 P_AAB65239 Human PRO1107 (UNQ550) protein sequence SEQ ID NO:285 - Homo (477 aa) [1 seg]
Score = 2561 (991 bits), Expect = 0.0
Identities = 477/477 (100%), Positives = 477/477 (100%), at 1,1-477,477

```
DNA59606.nc      1 MTSKFILVSFILAAALSLSTTFSLQLDQQKVLLVSFDGFRWDYLYKVPTPHFHYIMKYGVH
*****
P_AAB65239       1 MTSKFILVSFILAAALSLSTTFSLQLDQQKVLLVSFDGFRWDYLYKVPTPHFHYIMKYGVH

DNA59606.nc     61 VKQVTNVFITKTYPNHYTLVTGLFAENHGIVANDMFDPIRNKSFSLDHMNIYDSKFWEEA
*****
P_AAB65239      61 VKQVTNVFITKTYPNHYTLVTGLFAENHGIVANDMFDPIRNKSFSLDHMNIYDSKFWEEA

DNA59606.nc    121 TPIWITNQRAGHTSGAAMWPGTDVKIHKRFPTHYMPYNESVSFEDRVAKIVWFSTKEPI
*****
P_AAB65239    121 TPIWITNQRAGHTSGAAMWPGTDVKIHKRFPTHYMPYNESVSFEDRVAKIVWFSTKEPI

DNA59606.nc    181 NLGLLYWEDPDDMGHHLGPDSPLMGPVISDIDKKLGYLIQMLKKAKLWNTLNLIITSDHG
*****
P_AAB65239    181 NLGLLYWEDPDDMGHHLGPDSPLMGPVISDIDKKLGYLIQMLKKAKLWNTLNLIITSDHG

DNA59606.nc    241 MTQCSEERLIELDQYLDKDHYTELIDQSPVAAILPKEGKFDEVYEALTHAHPNLTVYKKED
*****
P_AAB65239    241 MTQCSEERLIELDQYLDKDHYTELIDQSPVAAILPKEGKFDEVYEALTHAHPNLTVYKKED

DNA59606.nc    301 VPERWHYKYNSRIQPIIAVADEGWHLQNKSDDFLLGNHGYDNALADMHPIFLAHGPAFR
*****
P_AAB65239    301 VPERWHYKYNSRIQPIIAVADEGWHLQNKSDDFLLGNHGYDNALADMHPIFLAHGPAFR

DNA59606.nc    361 KNFSKEAMNSTDLYPDLLCHLLNITAMPHNGSFWNVQDLLNSAMPRVVPYTQSTILLPGSV
*****
P_AAB65239    361 KNFSKEAMNSTDLYPDLLCHLLNITAMPHNGSFWNVQDLLNSAMPRVVPYTQSTILLPGSV

DNA59606.nc    421 KPAEYDQEGSYPYFIGVSLGSIIVIVFFVIFIKHLIHSQIPALQDMHAEIAQPLLQA
*****
P_AAB65239    421 KPAEYDQEGSYPYFIGVSLGSIIVIVFFVIFIKHLIHSQIPALQDMHAEIAQPLLQA
```

>2 P_AAU12397 Human PRO1107 polypeptide sequence - Homo sapiens. (477 aa) [1 seg]
Score = 2561 (991 bits), Expect = 0.0

BLAST RESULTS B-2

Identities = 477/477 (100%), Positives = 477/477 (100%), at 1,1-477,477

```
DNA59606.nc      1 MTSKFILVSFILAALSLSTTFSLQLDQQKVLLVSFDGFRWDYLYKVPTPHFHYIMKYGVH
*****
P_AAU12397      1 MTSKFILVSFILAALSLSTTFSLQLDQQKVLLVSFDGFRWDYLYKVPTPHFHYIMKYGVH

DNA59606.nc     61 VKQVTNVFITKTYPNHYTLVTGLFAENHGIVANDMFDPIRNKSFSLDHMNIYDSKFWEEA
*****
P_AAU12397     61 VKQVTNVFITKTYPNHYTLVTGLFAENHGIVANDMFDPIRNKSFSLDHMNIYDSKFWEEA

DNA59606.nc    121 TPIWITNQRAGHTSGAAMWPGTDVKIHKRFPTHYMPYNESVSFEDRVAKIVEWFTSKEPI
*****
P_AAU12397    121 TPIWITNQRAGHTSGAAMWPGTDVKIHKRFPTHYMPYNESVSFEDRVAKIVEWFTSKEPI

DNA59606.nc    181 NLGLLYWEDPDDMGHHLGPDSPLMGPVISDIDKKLGYLIQMLKKAKLWNTLNLIITS DHG
*****
P_AAU12397    181 NLGLLYWEDPDDMGHHLGPDSPLMGPVISDIDKKLGYLIQMLKKAKLWNTLNLIITS DHG

DNA59606.nc    241 MTQCSEERLIELDQYLDKDH TYTLIDQSPVAAILPKEGKFDEVYEAL THAHPNLT VYKKED
*****
P_AAU12397    241 MTQCSEERLIELDQYLDKDH TYTLIDQSPVAAILPKEGKFDEVYEAL THAHPNLT VYKKED

DNA59606.nc    301 VPERWHYKYNSRIQPIIAVADEGWHILQNKSDDFLLGNHGYDNALADMHPIFLAHGPAFR
*****
P_AAU12397    301 VPERWHYKYNSRIQPIIAVADEGWHILQNKSDDFLLGNHGYDNALADMHPIFLAHGPAFR

DNA59606.nc    361 KNFSKEAMNSTDLYPLLCHLLNITAMPHNGSFWNVQDLLNSAMPRVVPYTQSTILLPGSV
*****
P_AAU12397    361 KNFSKEAMNSTDLYPLLCHLLNITAMPHNGSFWNVQDLLNSAMPRVVPYTQSTILLPGSV

DNA59606.nc    421 KPAEYDQEGSYPYFIGVSLGSIIVIVFFVIFIKHLIHSQIPALQDMHAEIAQPLLQA
*****
P_AAU12397    421 KPAEYDQEGSYPYFIGVSLGSIIVIVFFVIFIKHLIHSQIPALQDMHAEIAQPLLQA
```

>3 P_AAY66716 Membrane-bound protein PRO1107 - Homo sapiens. (477 aa) [1 seg]
Score = 2561 (991 bits), Expect = 0.0
Identities = 477/477 (100%), Positives = 477/477 (100%), at 1,1-477,477

```
DNA59606.nc      1 MTSKFILVSFILAALSLSTTFSLQLDQQKVLLVSFDGFRWDYLYKVPTPHFHYIMKYGVH
*****
P_AAY66716      1 MTSKFILVSFILAALSLSTTFSLQLDQQKVLLVSFDGFRWDYLYKVPTPHFHYIMKYGVH

DNA59606.nc     61 VKQVTNVFITKTYPNHYTLVTGLFAENHGIVANDMFDPIRNKSFSLDHMNIYDSKFWEEA
*****
P_AAY66716     61 VKQVTNVFITKTYPNHYTLVTGLFAENHGIVANDMFDPIRNKSFSLDHMNIYDSKFWEEA

DNA59606.nc    121 TPIWITNQRAGHTSGAAMWPGTDVKIHKRFPTHYMPYNESVSFEDRVAKIVEWFTSKEPI
*****
P_AAY66716    121 TPIWITNQRAGHTSGAAMWPGTDVKIHKRFPTHYMPYNESVSFEDRVAKIVEWFTSKEPI

DNA59606.nc    181 NLGLLYWEDPDDMGHHLGPDSPLMGPVISDIDKKLGYLIQMLKKAKLWNTLNLIITS DHG
*****
P_AAY66716    181 NLGLLYWEDPDDMGHHLGPDSPLMGPVISDIDKKLGYLIQMLKKAKLWNTLNLIITS DHG

DNA59606.nc    241 MTQCSEERLIELDQYLDKDH TYTLIDQSPVAAILPKEGKFDEVYEAL THAHPNLT VYKKED
*****
P_AAY66716    241 MTQCSEERLIELDQYLDKDH TYTLIDQSPVAAILPKEGKFDEVYEAL THAHPNLT VYKKED
```

Blast Results B-3

```
DNA59606.nc 301 VPERWHYKYSRIQPIIAVADEGWHILQNKSDDFLLGNHGYDNALADMHPIFLAHGPAFR
*****
P_AAY66716 301 VPERWHYKYSRIQPIIAVADEGWHILQNKSDDFLLGNHGYDNALADMHPIFLAHGPAFR

DNA59606.nc 361 KNFSKEAMNSTDLYPLLCHLLNITAMPHNGSFWNVQDLLNSAMPRVVPYTQSTILLPGSV
*****
P_AAY66716 361 KNFSKEAMNSTDLYPLLCHLLNITAMPHNGSFWNVQDLLNSAMPRVVPYTQSTILLPGSV

DNA59606.nc 421 KPAEYDQEGSYPYFIGVSLGSIIVIVFFVIFIKHLIHSQIPALQDMHAEIAQPLLQA
*****
P_AAY66716 421 KPAEYDQEGSYPYFIGVSLGSIIVIVFFVIFIKHLIHSQIPALQDMHAEIAQPLLQA
```

>4 P_AAB24072 Human PRO1107 protein sequence SEQ ID NO:44 - Homo sapiens. (477 aa) [1 seg]

Score = 2561 (991 bits), Expect = 0.0

Identities = 477/477 (100%), Positives = 477/477 (100%), at 1,1-477,477

```
DNA59606.nc 1 MTSKFILVSFILAALSLSTTFSLQLDQQKVLVVSFDGFRWDYLYKVPTPHFHYIMKYGVH
*****
P_AAB24072 1 MTSKFILVSFILAALSLSTTFSLQLDQQKVLVVSFDGFRWDYLYKVPTPHFHYIMKYGVH

DNA59606.nc 61 VKQVTNVFITKTYPNHYTLVTGLFAENHGIVANDMFDPIRNKSFSLDHMNIYDSKFWEEA
*****
P_AAB24072 61 VKQVTNVFITKTYPNHYTLVTGLFAENHGIVANDMFDPIRNKSFSLDHMNIYDSKFWEEA

DNA59606.nc 121 TPIWITNQRAGHTSGAAMWPGTDVKIHKRFPTHYMPYNESVSFEDRVAKIVWFTSKEPI
*****
P_AAB24072 121 TPIWITNQRAGHTSGAAMWPGTDVKIHKRFPTHYMPYNESVSFEDRVAKIVWFTSKEPI

DNA59606.nc 181 NLGLLYWEDPDDMGHHLGPDSPLMGPVISDIDKKLGYLIQMLKKAKLWNTLNLIITSDHG
*****
P_AAB24072 181 NLGLLYWEDPDDMGHHLGPDSPLMGPVISDIDKKLGYLIQMLKKAKLWNTLNLIITSDHG

DNA59606.nc 241 MTQCSEERLIELDQYLDKDHHTLIDQSPVAAILPKEGKFDEVYEALTHAHPNLTIVYKKED
*****
P_AAB24072 241 MTQCSEERLIELDQYLDKDHHTLIDQSPVAAILPKEGKFDEVYEALTHAHPNLTIVYKKED

DNA59606.nc 301 VPERWHYKYSRIQPIIAVADEGWHILQNKSDDFLLGNHGYDNALADMHPIFLAHGPAFR
*****
P_AAB24072 301 VPERWHYKYSRIQPIIAVADEGWHILQNKSDDFLLGNHGYDNALADMHPIFLAHGPAFR

DNA59606.nc 361 KNFSKEAMNSTDLYPLLCHLLNITAMPHNGSFWNVQDLLNSAMPRVVPYTQSTILLPGSV
*****
P_AAB24072 361 KNFSKEAMNSTDLYPLLCHLLNITAMPHNGSFWNVQDLLNSAMPRVVPYTQSTILLPGSV

DNA59606.nc 421 KPAEYDQEGSYPYFIGVSLGSIIVIVFFVIFIKHLIHSQIPALQDMHAEIAQPLLQA
*****
P_AAB24072 421 KPAEYDQEGSYPYFIGVSLGSIIVIVFFVIFIKHLIHSQIPALQDMHAEIAQPLLQA
```

>5 P_AAE05491 Human phosphodiesterase-1 (HPDE-1) - Homo sapiens. (477 aa) [1 seg]

Score = 2553 (988 bits), Expect = 0.0

Identities = 475/477 (99%), Positives = 476/477 (99%), at 1,1-477,477

```
DNA59606.nc 1 MTSKFILVSFILAALSLSTTFSLQLDQQKVLVVSFDGFRWDYLYKVPTPHFHYIMKYGVH
*****
```

P_AAE05491 1 MTSKFILVSFILAALSLSTTFSLQPDQQKVLVSFDGFRWDYLYKVPTPHFHYIMKYGVH

DNA59606.nc 61 VKQVTNVFITKTYPNHYTLVTGLFAENHGIVANDMFDPIRNKSFSLDHMNIYDSKFWEEA

P_AAE05491 61 VKQVTNVFITKTYPNHYTLVTGLFAENHGIVANDMFDPIRNKSFSLDHMNIYDSKFWEEA

DNA59606.nc 121 TPIWITNQRAGHTSGAAMWPGTDVKIHKRFPTHYMPYNESVSFEDRVAKIVWFSTKEPI

P_AAE05491 121 TPIWITNQRAGHTSGAAMWPGTDVKIHKRFPTHYMPYNESVSFEDRVAKIIEWFSTKEPI

DNA59606.nc 181 NLGLLYWEDPDDMGHHLGPDSPLMGPVISDIDKKLGYLIQMLKKAKLWNTLNLIITSDHG

P_AAE05491 181 NLGLLYWEDPDDMGHHLGPDSPLMGPVISDIDKKLGYLIQMLKKAKLWNTLNLIITSDHG

DNA59606.nc 241 MTQCSEERLIELDQYLDKDHYTELIDQSPVAAILPKEGKFDEVYEALTHAHPNLTVYKKED

P_AAE05491 241 MTQCSEERLIELDQYLDKDHYTELIDQSPVAAILPKEGKFDEVYEALTHAHPNLTVYKKED

DNA59606.nc 301 VPERWHYKYNRIQPIIAVADEGWHILQNKSDDFLLGNHGYDNALADMHPIFLAHGPAFR

P_AAE05491 301 VPERWHYKYNRIQPIIAVADEGWHILQNKSDDFLLGNHGYDNALADMHPIFLAHGPAFR

DNA59606.nc 361 KNFSKEAMNSTDLYPDLLCHLLNITAMPHNGSFWNVQDLLNSAMPRVVPYTQSTILLPGSV

P_AAE05491 361 KNFSKEAMNSTDLYPDLLCHLLNITAMPHNGSFWNVQDLLNSAMPRVVPYTQSTILLPGSV

DNA59606.nc 421 KPAEYDQEGSYPYFIGVSLGSIIVIVFFVIFIKHLIHSQIPALQDMHAEIAQPLLQA

P_AAE05491 421 KPAEYDQEGSYPYFIGVSLGSIIVIVFFVIFIKHLIHSQIPALQDMHAEIAQPLLQA

>6 CAB56566.1 dJ8B1.3 (similar to PLASMA-CELL MEMBRANE GLYCOPROTEIN PC-1) - Homo sapiens (477 aa) [1 seg]
Score = 2551 (987 bits), Expect = 0.0
Identities = 474/477 (99%), Positives = 476/477 (99%), at 1,1-477,477.

DNA59606.nc 1 MTSKFILVSFILAALSLSTTFSLQPDQQKVLVSFDGFRWDYLYKVPTPHFHYIMKYGVH

CAB56566.1 1 MTSKFLLVSFILAALSLSTTFSLQPDQQKVLVSFDGFRWDYLYKVPTPHFHYIMKYGVH

DNA59606.nc 61 VKQVTNVFITKTYPNHYTLVTGLFAENHGIVANDMFDPIRNKSFSLDHMNIYDSKFWEEA

CAB56566.1 61 VKQVTNVFITKTYPNHYTLVTGLFAENHGIVANDMFDPIRNKSFSLDHMNIYDSKFWEEA

DNA59606.nc 121 TPIWITNQRAGHTSGAAMWPGTDVKIHKRFPTHYMPYNESVSFEDRVAKIVWFSTKEPI

CAB56566.1 121 TPIWITNQRAGHTSGAAMWPGTDVKIHKRFPTHYMPYNESVSFEDRVAKIIEWFSTKEPI

DNA59606.nc 181 NLGLLYWEDPDDMGHHLGPDSPLMGPVISDIDKKLGYLIQMLKKAKLWNTLNLIITSDHG

CAB56566.1 181 NLGLLYWEDPDDMGHHLGPDSPLMGPVISDIDKKLGYLIQMLKKAKLWNTLNLIITSDHG

DNA59606.nc 241 MTQCSEERLIELDQYLDKDHYTELIDQSPVAAILPKEGKFDEVYEALTHAHPNLTVYKKED

CAB56566.1 241 MTQCSEERLIELDQYLDKDHYTELIDQSPVAAILPKEGKFDEVYEALTHAHPNLTVYKKED

DNA59606.nc 301 VPERWHYKYNRIQPIIAVADEGWHILQNKSDDFLLGNHGYDNALADMHPIFLAHGPAFR

Blast results B-A

Blast Results 2-5

```
CAB56566.1 301 VPERWHYKYNRIQPIIAVADEGWHLQNKSDDFLLGNHGYDNALADMHPIFLAHGPAFR
DNA59606.nc 361 KNFSKEAMNSTDLYPLLCHLLNITAMPHNGSFWNVQDLLNSAMPRVVPYTQSTILLPGSV
*****
CAB56566.1 361 KNFSKEAMNSTDLYPLLCHLLNITAMPHNGSFWNVQDLLNSAMPRVVPYTQSTILLPGSV
DNA59606.nc 421 KPAEYDQEGSYPYFIGVSLGSIIVIVFFVIFIKHLIHSQIPALQDMHAEIAQPLLQA
*****
CAB56566.1 421 KPAEYDQEGSYPYFIGVSLGSIIVIVFFVIFIKHLIHSQIPALQDMHAEIAQPLLQA
```

>7 NP_067547.1 ectonucleotide pyrophosphatase/phosphodiesterase 5 (putative function) - Homo sapiens (477 aa) [1 seg]
Score = 2551 (987 bits), Expect = 0.0
Identities = 474/477 (99%), Positives = 476/477 (99%), at 1,1-477,477

```
DNA59606.nc 1 MTSKFILVSFILAALSSTTFSLQLDQQKVLLVSFDGFRWDYLYKVPTPHFHYIMKYGVH
*****
NP_067547.1 1 MTSKFLLVSFILAALSSTTFSLQPDQQKVLLVSFDGFRWDYLYKVPTPHFHYIMKYGVH
DNA59606.nc 61 VKQVTNVFITKTYPNHYTLVTGLFAENHGIVANDMFDPIRNKSFSLDHMNIYDSKFWEEA
*****
NP_067547.1 61 VKQVTNVFITKTYPNHYTLVTGLFAENHGIVANDMFDPIRNKSFSLDHMNIYDSKFWEEA
DNA59606.nc 121 TPIWITNQRAGHTSGAAMWPGTDVKIHKRFPTHYMPYNESVSFEDRVAKIIEWFTSKEPI
*****
NP_067547.1 121 TPIWITNQRAGHTSGAAMWPGTDVKIHKRFPTHYMPYNESVSFEDRVAKIIEWFTSKEPI
DNA59606.nc 181 NLGLLYWEDPDDMGHHLGPDSPMLGPGVISDIDKKLGYLIQMLKKAKLWNTLNLIITSDHG
*****
NP_067547.1 181 NLGLLYWEDPDDMGHHLGPDSPMLGPGVISDIDKKLGYLIQMLKKAKLWNTLNLIITSDHG
DNA59606.nc 241 MTQCSEERLIELDQYLDKDHYTELIDQSPVAAILPKEGKFDEVYEALTHAHPNLTVYKKED
*****
NP_067547.1 241 MTQCSEERLIELDQYLDKDHYTELIDQSPVAAILPKEGKFDEVYEALTHAHPNLTVYKKED
DNA59606.nc 301 VPERWHYKYNRIQPIIAVADEGWHLQNKSDDFLLGNHGYDNALADMHPIFLAHGPAFR
*****
NP_067547.1 301 VPERWHYKYNRIQPIIAVADEGWHLQNKSDDFLLGNHGYDNALADMHPIFLAHGPAFR
DNA59606.nc 361 KNFSKEAMNSTDLYPLLCHLLNITAMPHNGSFWNVQDLLNSAMPRVVPYTQSTILLPGSV
*****
NP_067547.1 361 KNFSKEAMNSTDLYPLLCHLLNITAMPHNGSFWNVQDLLNSAMPRVVPYTQSTILLPGSV
DNA59606.nc 421 KPAEYDQEGSYPYFIGVSLGSIIVIVFFVIFIKHLIHSQIPALQDMHAEIAQPLLQA
*****
NP_067547.1 421 KPAEYDQEGSYPYFIGVSLGSIIVIVFFVIFIKHLIHSQIPALQDMHAEIAQPLLQA
```

>8 A59391 probable phosphodiesterase I (EC 3.1.4.1) / nucleotide pyrophosphatase (EC 3.6.1.9) 5 - human (477 aa) [1 seg]
Score = 2551 (987 bits), Expect = 0.0
Identities = 474/477 (99%), Positives = 476/477 (99%), at 1,1-477,477

```
DNA59606.nc 1 MTSKFILVSFILAALSSTTFSLQLDQQKVLLVSFDGFRWDYLYKVPTPHFHYIMKYGVH
*****
A59391 1 MTSKFLLVSFILAALSSTTFSLQPDQQKVLLVSFDGFRWDYLYKVPTPHFHYIMKYGVH
DNA59606.nc 61 VKQVTNVFITKTYPNHYTLVTGLFAENHGIVANDMFDPIRNKSFSLDHMNIYDSKFWEEA
```

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*****
A59391      61 VKQVTNVFITKTYPNHYTLVTGLFAENHGIVANDMFDPIRNKSFSLDHMNIYDSKFWEEA
DNA59606.nc 121 TPIWITNQRAGHTSGAAMWPGTDVKIHKRFPTHYMPYNESVSFEDRVAKIIEWFTSKEPI
*****
A59391      121 TPIWITNQRAGHTSGAAMWPGTDVKIHKRFPTHYMPYNESVSFEDRVAKIIEWFTSKEPI
DNA59606.nc 181 NLGLLYWEDPDDMGHHLGPDSPLMGPVISDIDKKLGYLIQMLKKAKLWNTLNLIITSDHG
*****
A59391      181 NLGLLYWEDPDDMGHHLGPDSPLMGPVISDIDKKLGYLIQMLKKAKLWNTLNLIITSDHG
DNA59606.nc 241 MTQCSEERLIELDQYLDKDHHTLIDQSPVAAILPKEGKFDEVYEALTAHPNLTVYKKED
*****
A59391      241 MTQCSEERLIELDQYLDKDHHTLIDQSPVAAILPKEGKFDEVYEALTAHPNLTVYKKED
DNA59606.nc 301 VPERWHYKYSRIQPIIAVADEGWHILQNKSDDFLLGNHGYDNALADMHPIFLAHGPAFR
*****
A59391      301 VPERWHYKYSRIQPIIAVADEGWHILQNKSDDFLLGNHGYDNALADMHPIFLAHGPAFR
DNA59606.nc 361 KNFSKEAMNSTDLYPLLCHLLNITAMPNGSFWNVQDLLNSAMPRVVPYTQSTILLPGSV
*****
A59391      361 KNFSKEAMNSTDLYPLLCHLLNITAMPNGSFWNVQDLLNSAMPRVVPYTQSTILLPGSV
DNA59606.nc 421 KPAEYDQEGSYPIFYGVSLGSIIVIVFFVIFIKHLIHSQIPALQDMHAEIAQPLLQA
*****
A59391      421 KPAEYDQEGSYPIFYGVSLGSIIVIVFFVIFIKHLIHSQIPALQDMHAEIAQPLLQA

>9 P_AAM23765 Human EST encoded protein SEQ ID NO: 1290 - Homo sapiens. (452 aa)
[1 seg]
Score = 2403 (930 bits), Expect = 0.0
Identities = 446/451 (98%), Positives = 447/451 (98%), at 1,1-451,451

DNA59606.nc      1 MTSKFILVSFILAALSSTTFSLQDQQKVLVSFDGFRWDYLYKVPTPHFHYIMKYGVH
*****
P_AAM23765       1 MTSKFILVSFILAALSSTTFSLQDQQKVLVSFDGFRWDYLYKVPTPHFHYIMKYGVH
DNA59606.nc     61 VKQVTNVFITKTYPNHYTLVTGLFAENHGIVANDMFDPIRNKSFSLDHMNIYDSKFWEEA
*****
P_AAM23765      61 VKQVTNVFITKTYPNHYTLVTGLFAENHGIVANDMFDPIRNKSFSLDHMNIYDSKFWEEA
DNA59606.nc    121 TPIWITNQRAGHTSGAAMWPGTDVKIHKRFPTHYMPYNESVSFEDRVAKIIEWFTSKEPI
*****
P_AAM23765     121 TPIWITNQRAGHTSGAAMWPGTDVKIHKRFPTHYMPYNESVSFEDRVAKIIEWFTSKEPI
DNA59606.nc    181 NLGLLYWEDPDDMGHHLGPDSPLMGPVISDIDKKLGYLIQMLKKAKLWNTLNLIITSDHG
*****
P_AAM23765     181 NLGLLYWEDPDDMGHHLGPDSPLMGPVISDIDKKLGYLIQMLKKAKLWNTLNLIITSDHG
DNA59606.nc    241 MTQCSEERLIELDQYLDKDHHTLIDQSPVAAILPKEGKFDEVYEALTAHPNLTVYKKED
*****
P_AAM23765     241 MTQCSEERLIELDQYLDKDHHTLIDQSPVAAILPKEGKFDEVYEALTAHPNLTVYKKED
DNA59606.nc    301 VPERWHYKYSRIQPIIAVADEGWHILQNKSDDFLLGNHGYDNALADMHPIFLAHGPAFR
*****
P_AAM23765     301 VPERWHYKYSRIQPIIAVADEGWHILQNKSDDFLLGNHGYDNALADMHPIFLAHGPAFR
DNA59606.nc    361 KNFSKEAMNSTDLYPLLCHLLNITAMPNGSFWNVQDLLNSAMPRVVPYTQSTILLPGSV

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BLAST RESULTS B-U

```
*****
P_AAM23765 361 KNFSKEAMNSTDLYPLLCHLLNITAMPHNGSFWNVQDLLNSAMPRVVPYTQSTILLPGSV
DNA59606.nc 421 KPAEYDQEGSYPHYFIGVSLGSIIVIVFFVIF
*****
P_AAM23765 421 KPAEYDQEGSYPHYFIGVSLGSIIVIVFFCNF
```

Blast Results B-7